B. Whiteman

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1635

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,678A

DATE: 04/10/2002
TIME: 09:30:51

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Output Set: **N:\CRF3\04102002\I964678A.raw**

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 1 <110> APPLICANT: de la Monte, Suzanne
 2        Wands, Jack R.
 3 <120> TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs
 4        Effective for the Treatment or Prevention of
 5        Alzheimer's Disease
 6 <130> FILE REFERENCE: 0609.4370002
C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/964,678A
 8 <141> CURRENT FILING DATE: 2001-09-28
 9 <150> PRIOR APPLICATION NUMBER: 09/380,203
10 <151> PRIOR FILING DATE: 2000-04-25
11 <150> PRIOR APPLICATION NUMBER: PCT/US98/03685
12 <151> PRIOR FILING DATE: 1998-02-26
13 <150> PRIOR APPLICATION NUMBER: 60/038,908
14 <151> PRIOR FILING DATE: 1997-02-26
15 <160> NUMBER OF SEQ ID NOS: 14
16 <170> SOFTWARE: PatentIn version 3.1
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20 <212> TYPE: DNA
21 <213> ORGANISM: Unknown
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25 <222> LOCATION: (15)..(1139)
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             Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
29                        1               5                   10
30        aat ggc gca atc tca gct cac cgc aac ctc cgc ctc ccg ggt tca agc      98
31        Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser
32                    15                  20                  25
33        gat tct cct gcc tca gcc tcc cca gta gct ggg att aca ggc atg tgc     146
34        Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys
35                30                  35                  40
36        acc cac gct cgg cta att ttg tat ttt ttt tta gta gag atg gag ttt     194
37        Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe
38                45                  50                  55                  60
39        ctc cat gtt ggt cag gct ggt ctc gaa ctc ccg acc tca gat gat ccc     242
40        Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro
41                            65                  70                  75
42        tcc gtc tcg gcc tcc caa agt gct aga tac agg act ggc cac cat gcc     290
43        Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala
44
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file://C:\Crf3\Outhold\VsrI964678A.htm

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45                      80                      85                      90
46    cgg ctc tgc ctg gct aat ttt tgt ggt aga aac agg gtt tca ctg atg    338
47    Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met
48            95                     100                     105
49    tgc cca agc tgg tct cct gag ctc aag cag tcc acc tgc ctc agc ctc    386
50    Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu
51           110                     115                     120
52    cca aag tgc tgg gat tac agg cgt gca gcc gtg cct ggc ctt ttt att    434
53    Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile
54          125                     130                     135           140
55    tta ttt ttt tta aga cac agg tgt ccc act ctt acc cag gat gaa gtg    482
56    Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val
57                         145                     150                     155
58    cag tgg tgt gat cac agc tca ctg cag cct tca act cct gag atc aag    530
59    Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys
60                         160                     165             170
61    cat cct cct gcc tca gcc tcc caa gta gct ggg acc aaa gac atg cac    578
62    His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His
63                 175                     180                     185
64    cac tac acc tgg cta att ttt att ttt att ttt aat ttt ttg aga cag    626
65    His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln
66            190                     195                     200
67    agt ctc aac tct gtc acc cag gct gga gtg cag tgg cgc aat ctt ggc    674
68    Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly
69            205                     210                     215             220
70    tca ctg caa cct ctg cct ccc ggg ttc aag tta ttc tcc tgc ccc agc    722
71    Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser
72                         225                     230                     235
73    ctc ctg agt agc tgg gac tac agg cgc cca cca cgc cta gct aat ttt    770
74    Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe
75                         240                     245             250
76    ttt gta ttt tta gta gag atg ggg ttc acc atg ttc gcc agg ttg atc    818
77    Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile
78                 255                     260                     265
79    ttg atc tct gga cct tgt gat ctg cct gcc tcg gcc tcc caa agt gct    866
80    Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala
81            270                     275                     280
82    ggg att aca ggc gtg agc cac cac gcc cgg ctt att ttt aat ttt tgt    914
83    Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys
84            285                     290                     295             300
85    ttg ttt gaa atg gaa tct cac tct gtt acc cag gct gga gtg caa tgg    962
86    Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp
87                         305                     310                     315
88    cca aat ctc ggc tca ctg caa cct ctg cct ccc ggg ctc aag cga ttc    1010
89    Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe
90                 320                     325                     330
91    tcc tgt ctc agc ctc cca agc agc tgg gat tac ggg cac ctg cca cca    1058
92    Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro
93                 335                     340                     345
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94        cac ccc gct aat ttt tgt att ttc att aga ggc ggg gtt tca cca tat      1106
95        His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr
96            350                 355                 360
97        ttg tca ggc tgg tct caa act cct gac ctc agg tgacccacct gcctcagcct      1159
98        Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg
99            365                 370                 375
100        tccaaagtgc tgggattaca ggcgtgagcc acctcaccca gccggctaat ttagataaaa      1219
101        aaatatgtag caatggggggg tcttgctatg ttgcccaggc tggtctcaaa cttctggctt     1279
102        catgcaatcc ttccaaatga gccacaacac ccagccagtc acatttttta aacagttaca      1339
103        tctttatttt agtatactag aaagtaatac aataaacatg tcaaacctgc aaattcagta      1399
104        gtaacagagt cttttataaa cttttaaaca aagctttaga gca                        1442
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108  <212> TYPE: PRT
109  <213> ORGANISM: Unknown
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115        Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala
116                    20                  25                  30
117        Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
118                    35                  40                  45
119        Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
120            50                  55                  60
121        Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
122        65                  70                  75                  80
123        Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
124                        85                  90                  95
125        Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
126                    100                 105                 110
127        Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
128                    115                 120                 125
129        Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
130                    130                 135                 140
131        Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
132        145                 150                 155                 160
133        His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
134                        165                 170                 175
135        Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
136                    180                 185                 190
137        Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
138                    195                 200                 205
139        Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
140                    210                 215                 220
141        Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
142        225                 230                 235                 240
143        Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
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                              245                 250                 255
144
145        Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
146                        260                 265                 270
147        Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
148                        275                 280                 285
149        Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
150                        290                 295                 300
151        Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
152        305                 310                 315                 320
153        Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
154                        325                 330                 335
155        Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
156                        340                 345                 350
157        Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
158                        355                 360                 365
159        Ser Gln Thr Pro Asp Leu Arg
160                        370                 375
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162 <210> SEQ ID NO: 3
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164 <212> TYPE: DNA
165 <213> ORGANISM: Unknown
166 <220> FEATURE:
167 <223> OTHER INFORMATION: Incorrect sequence of AD7c-NTP DNA
168 <400> SEQUENCE: 3

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171    agtagctggg attacaggca tgtgcaccac gctcggctaa tttttgtattt ttttttagta    180
172    gagatggagt ttaactccat gttggtcagg ctggtctcga actcccgacc tcagatgatc     240
173    tcccgtctcg gcctgcccaa agtgctgaga ttacaggcat gagccaccat gcccggcctc     300
174    tgcctggcta attttgtgg tagaaacagg gtttcactga tgttgcccaa gctggtctcc      360
175    tgagctcaag cagtccacct gcctcagcct cccaaagtgc tgggattaca ggcgtcagcc     420
176    gtgcctggcc tttttatttt attttttta agacacaggt gtaccactct tacccaggat      480
177    gaagtgcagt ggtgtgatca cagctcactg cagccttcaa ctcctgagat caagcaatcc     540
178    tcctgcctca gcctcccaag tagctgggac caaagacatg caccactaca cctggtaatt     600
179    tttattttta tttttaattt tttgagacag agtctcactc tgtcacccag gctggagtgc     660
180    agtggcgcaa tcttggctca ctgcaacctc tgcctcccgg gttcaagtta ttctcctgcc     720
181    ccagcctcct gagtagctgg gactacaggc gcccaccacg cctagctaat tttttgtat     780
182    ttttagtaga gatggggttt caccatgttc gccaggttga tcttgatctc ttgaccttgt     840
183    gatctgcctg cctcggccta cccaaagtgc tgggattaca ggtcgtgact ccacgccggc     900
184    ctattttaa ttttgtttg tttgaaatgg aatctcactc tgttacccag gtcggagtgc      960
185    aatggcaaat ctcggctact cgcaacctct gcctcccggg tcaagcgatt ctcctgtctc    1020
186    agcctcccaa gcagctggga ttacgggacc tgcaccacac cccgctaatt tttgtatttt    1080
187    cattagaggc gggtttacca tatttgtcag ctgggtctc aaactcctga cctcaggtga    1140
188    cccacctgcc tcagccttcc aaagtgctgg gattacaggc gtgagccacc tcacccagcc    1200
189    ggctaatttg gaataaaaaa tatgtagcaa tgggggtctg ctatgttgcc caggctggtc    1260
190    tcaaacttct ggcttcagtc aatccttcca aatgagccac aacacccagc cagtcacatt    1320
191    ttttaaacag ttacatcttt attttagtat actagaaagt aatacaataa acatgtcaaa    1380
192    c                                                                    1381
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197 <213> ORGANISM: Unknown
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Incorrect sequence of AD7c-NTP cDNA
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203      agtaggctgg gattacaggc atgtgcacca cgctcggcta attttgtatt tttttttagt     180
204      agagatggag tttctccatg ttggtcaggc tggtctcgaa ctccgacctc agatgatcct     240
205      cccgtctcgg cctcccaaag tgctagatac aggactgagc accatgcccg gcctctgcct     300
206      ggctaatttt tgtggtagaa acagggtttc actgatgtgc ccaagctggt ctcctgagct     360
207      caagcagtcc acctgcctca gcctcccaaa gtgctgggat tacaggcgtg cagccgtgcc     420
208      tggccttttt attttatttt ttttaagaca caggtgtccc actcttaccc aggatgaagt     480
209      gcagtggtgt gatcacagct cactgcagcc ttcaactctg agatcaagca tcctcctgcc     540
210      tcagcctccc aaagtagctg ggaccaaaga catgcaccac tacacctggc taattttat     600
211      ttttattttt aattttttga gacagagtct caactctgtc acccaggctg gagtgcagtg     660
212      gcgcaatctt ggctcactgc aacctctgcc tcccgggttc aagttattct cctgccccag     720
213      cctcctgagt agctgggact acaggcgccc accacgccta gctaattttt ttgtattttt     780
214      agtagagatg gggtttcacc atgttcgcca ggttgatgct agatctcttg accttgtgat     840
215      ctgcctgcct cggcctccca aagtgctggg attacaggac gtgacgccca ccgcccggcc     900
216      tattttaat ttttgtttgt ttgaaatgga atctcactct gttacccagg ctggagtgca     960
217      atggccaaat ctcggctcac tgcaacctct gcctcccggg ctcaagcgat tctcctgtct    1020
218      cagcctccca agcagctggg attacgggca cctgcaccac accccgctaa ttttttgtatt    1080
219      ttcattagag gcggggtttc accatatttg tcaggctggt ctcaaactcc tgacctcagg    1140
220      tgacccacct gcctcagcct tccaaagtgc tgggattaca ggcgtgacgc ctcacccagc    1200
221      cggctaattt agataaaaaa atatgtagca atggggggtc ttgctatgtt gcccaggctg    1260
222      gtctcaaact tctggcttca tgcaatcctt ccaaatgagc cacaacaccc agccagtcac    1320
223      attttttaaac agttacatct ttattttagt atactagaaa gtgatacgat aacatggcgg    1380
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228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: AD7c-NTP oligonucleotide
232 <400> SEQUENCE: 5                                                            22
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235 <210> SEQ ID NO: 6
236 <211> LENGTH: 24
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238 <213> ORGANISM: Artificial Sequence
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244 <210> SEQ ID NO: 7
245 <211> LENGTH: 20
246 <212> TYPE: DNA
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/10/2002
PATENT APPLICATION: US/09/964,678A   TIME: 09:30:53

Input Set : N:\paola\US09964678A.RAW
Output Set: N:\CRF3\04102002\I964678A.raw

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; N Pos. 11
Seq#:13; N Pos. 11
Seq#:14; N Pos. 11

VERIFICATION SUMMARY   DATE: 04/10/2002
PATENT APPLICATION: US/09/964,678A   TIME: 09:30:53

Input Set : **N:\paola\US09964678A.RAW**
Output Set: **N:\CRF3\04102002\I964678A.raw**

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L:24  M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:27  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:295 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:298 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:12
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:307 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:310 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:319 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:322 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14
L:323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
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